

REMARKS

Claims 8-10, 14-16, 18-20, and 22-24 are pending in the application, with Claims 1-7, 11-13, 17, 21, and 25-97 canceled in this amendment. The amendment to Claim 8 finds support in the specification and claims as originally filed, for example, at page 4, lines 3 and 10-20. No new matter is added by way of the amendments.

Applicants acknowledge the withdrawal of the grounds of rejection in the Office Action mailed March 21, 2002 (paper number 21).

Claims 8-10, 14-16, 18-20, and 22-24 stand rejected under 35 U.S.C. §102(e) as allegedly being anticipated by Kunsch et al., U.S. Patent 6,593,114. Applicants respectfully traverse the rejections, and note that Claims 10, 16, 20 and 24 were allowed in paper number 21 over EP 786519 to Kunsch et al., a foreign counterpart to U.S. Patent 6,593,114.

The Rejections Under 35 U.S.C. §102(e)

Claims 8-10, 14-16, 18-20, and 22-24 stand rejected under 35 U.S.C. §102(e), the Examiner suggesting that Kunsch et al., U.S. Patent 6,593,114 (hereafter "Kunsch") disclose "a polynucleotide represented by SEQ ID NO:538 which is 100% identical to the instantly claimed SEQ ID NO:2" (page 3, lines 20-21 of the Office Action). Presumably on this basis, the Examiner suggests that Kunsch disclose "Staphylococcus aureus polynucleotides, vectors comprising polynucleotides, host cells, and methods of recombinantly producing polypeptides."

Anticipation under 35 U.S.C. §102 requires that "every element of the claimed invention be identically shown in a single reference." (*In re Bond*, 910 F.2d 831,832 (Fed. Cir. 1990).

As defined in the specification at page 16, lines 14-16, "mismatch" "includes all unpaired bases when two nucleic acid sequences are hybridized with best alignment in the context of nucleic acid hybridization. If there is a mismatch, the sequences are not identical. One common way of detecting mismatches is to use one of the programs of the BLAST suite of programs to align and compare sequences. Such a comparison

provides a local, nucleotide by nucleotide comparison of the sequences, searching for the best alignments and determining the number of mismatches that remain even with the best alignment of the subject sequences.

As shown in the enclosed BLAST2 sequence comparison results, even with the best alignment, mismatches are found. In addition, a gap must be introduced into the sequence to provide this alignment; without the gap, the number of mismatches would be significantly greater. Thus, as determined by the BLAST2 comparison, SEQ ID NO:538 of Kunsch is NOT identical with SEQ ID NO:2 of the present application: the best BLAST alignment gives an identity of only 98%.

This is in agreement with the results of the previous comparison by the Examiner (Paper 19, page 8, line 11, dated 7/23/01) between SEQ ID NO: 2 and SEQ ID NO:538 as published in EP 786519: in that case, the Examiner also reported only 98% identity between the cited reference and the sequence of the present invention.

Thus, Applicants respectfully submit that SEQ ID NO:2 is not identical with SEQ ID NO: 538 of US Patent 6,593,114 and that the pending claims are not anticipated. Claim 10, and its dependent Claims 16, 20 and 24, are thus novel and not anticipated by the prior art.

Claims 8 and 9 recite amino acid sequences that are likewise not anticipated by the prior art. The amino acid sequence deduced from SEQ ID NO: 538 of Kunsch (although this amino acid sequence is never explicitly stated in Kunsch) includes 1165 amino acids, while SEQ ID NO: 3 of the present invention includes 205 amino acids. Kunsch fails to identify any portions of the amino acid sequence encoded by SEQ ID NO: 538; in particular, Kunsch fails to identify any 205 amino acid portion of the amino acid sequence encoded by SEQ ID NO: 538. Kunsch nowhere discloses the amino acid sequences of Claims 8 and 9. Having many more amino acids covalently joined together, so that selection, alignment and cleavage of the protein suggested by the nucleotide sequence of Kunsch must be performed in an attempt to provide the claimed

proteins, it is clear that the protein suggested by Kunsch is not identical to the claimed proteins, and does not anticipate the claimed invention.

Moreover, since Claims 8 and 9 are novel and not anticipated by the prior art, dependent Claims 14, 15, 18, 19, 22, and 23 are also are thus novel and not anticipated by the prior art.

Accordingly, Applicants submit that the rejections of Claims 8-10, 14-16, 18-20, and 22-24 under 35 U.S.C. §102(e) are overcome.

CONCLUSION

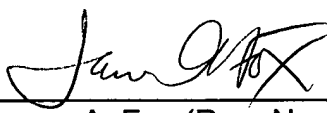
Applicants respectfully submit that all claim rejections are overcome by the above arguments, and request reconsideration and allowance of pending Claims 8-10, 14-16, 18-20 and 22-24. An early indication of allowance is earnestly requested.

The Commissioner is authorized to charge the fee for an extension of time of one month, and any additional fees, or credit any overpayment to Deposit Account No. **08-1641**, referencing Attorney's Docket No. **39754-0791 A**.

Respectfully submitted,

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By:


James A. Fox (Reg. No. 38,455)

Heller Ehrman White & McAuliffe LLP
275 Middlefield Road
Menlo Park, California 94025-3506
Telephone: (650) 324-6195
Facsimile: (650) 324-0638